

REPLACEMENT SHEET



Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu
1 5 10 15

Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His
20 25 30

Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
35 40 45

Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
50 55 60

Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
65 70 75 80

Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
85 90 95

Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
100 105 110

Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
115 120 125

Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
130 135 140

Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
145 150 155 160

Cys Arg Thr Gly Asp
165

FIG. 1

REPLACEMENT SHEET

Ala	Pro	Pro	Arg	Leu	Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg	Tyr	Leu
1				5					10					15	
Leu	Glu	Ala	Lys	Glu	Ala	Glu	Asn	Ile	Thr	Thr	Gly	Cys	Ala	Glu	His
	20							25					30		
Cys	Ser	Leu	Asn	Glu	Asn	Ile	Thr	Val	Pro	Asp	Thr	Lys	Val	Asn	Phe
	35						40					45			
Tyr	Ala	Trp	Lys	Arg	Met	Glu	Val	Gly	Gln	Gln	Ala	Val	Glu	Val	Trp
	50				55				60						
Gln	Gly	Leu	Ala	Leu	Leu	Ser	Glu	Ala	Val	Leu	Arg	Gly	Gln	Ala	Leu
	65					70				75			80		
Leu	Val	Asn	Ser	Ser	Gln	Pro	Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp
		85						90					95		
Lys	Ala	Val	Ser	Gly	Leu	Arg	Ser	Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu
		100						105					110		
Gly	Ala	Gln	Lys	Glu	Ala	Ile	Ser	Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala
		115					120				125				
Pro	Leu	Arg	Thr	Ile	Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val
		130					135			140					
Tyr	Ser	Asn	Phe	Leu	Arg	Gly	Lys	Leu	Lys	Leu	Tyr	Thr	Gly	Glu	Ala
		145				150			155				160		
Cys	Arg	Thr	Gly	Asp	Arg										
		165													

FIG. 2

REPLACEMENT SHEET

1 GGAATTCAACCACCATGGGGTGCACGAATGTCCTGCCTGGCTGTGGCTTCCTGTCCCT
 1-----+-----+-----+-----+-----+-----+ 60
 1 CCTTAAGTGGTGGTACCCCCACGTGCTTACAGGACGGACCCGAAGAGGGACAGGGA
 1 M G V H E C P A W L W L L S L -
 61 GCTGTCGCTCCCTCTGGGCTCCAGTCCTGGCGCCCCCCCCGAATCGAGGGCCGCGC
 61-----+-----+-----+-----+-----+-----+ 120
 61 CGACAGCGAGGGAGACCCGGAGGGTCAGGACCCCGGGGGGGGGCTTAGCTCCCGCGCG
 61 L S L P I G L P V L G A P P R I E G R A -
 121 CCCACCA CGCCTCATCTGTGACAGCCGAGTCCTGGAGAGGTACCTTGGAGGCCAAGGA
 121-----+-----+-----+-----+-----+-----+ 180
 121 GGGTGGTGC GGAGTAGACACTGTCGGCTCAGGACCTCTCCATGGAGAACCTCCGGTTCT
 121 P P R L I C D S R V L E R Y L L E A K E -
 181 GGCGAGAAATATCACGACGGCTGTGCTGAACACTGCAGCTTGAATGAGAATATCACTGT
 181-----+-----+-----+-----+-----+-----+ 240
 181 CCGGCTCTTATAGT GCTGCCCGACACGACTTGTGACGTCGAACTTACTCTTATAGT GACA
 181 A E N I T T G C A E H C S L N E N I T V -
 241 CCCAGACACCAAAAGTTAATTCTATGCCCTGGAAGAGGATGGAGGTGGCAGCAGGCCGT
 241-----+-----+-----+-----+-----+-----+ 300
 241 GGGTCTGTGGTTCAATTAAAGATA CGGACCTCTCCTACCTCCAGCCCGTCGTCCGGCA
 241 P D T K V N F Y A W K R M E V G Q Q A V -
 301 AGAAGTCTGGCAGGGCCTGGCCCTGCTGCGGAAGCTGTCTGCAGGCCAGGCCCTGTT
 301-----+-----+-----+-----+-----+-----+ 360
 301 TCTTCAGACCGTCCGGACCGGGACGACAGCCTTCGACAGGACGCCCGGTCCGGGACAA
 301 E V W Q G L A L L S E A V L R G Q A L L -
 361 GGTCAACTCTTCCCAGCCGTGGAGCCCTGCAGCTGCATGTGGATAAGCCGTAGTGG
 361-----+-----+-----+-----+-----+-----+ 420
 361 CCAGTTGAGAAGGGTCGGCACCCCTGGGGACGTCGACGTACACCTATTCGGCAGTCACC
 361 V N S S Q P W E P L Q L H V D K A V S G -
 421 CCTTCGCAGCCTCACCACTCTGCTTCGGCTCTGGAGCCAGAAGGAAGCCATCTCCCC
 421-----+-----+-----+-----+-----+-----+ 480
 421 GGAAGCGTCGGAGTGGTGAGACGAAGCCCGAGACCCCTGGGTCTTCCTCGGTAGAGGGG

FIG. 3a

REPLACEMENT SHEET

L R S L T T L L R A L G A Q K E A I S P -
TCCAGATGCGGCCCTCAGCTGCTCCACTCCGAACAAATCACTGCTGACACTTCCGAAACT
481 -----+-----+-----+-----+-----+-----+ 540

AGGTCTACGCCGGAGTCGACGAGGTGAGGCTTGTAGTGACGACTGTGAAAGGCGTTGA
P D A A S A A P L R T I T A D T F R K L -
CTTCCGAGTCTACTCCAATTCCCTCCGGGGAAAGCTGAAGCTGTACACAGGGGAGGCCTG
541 -----+-----+-----+-----+-----+-----+ 600

GAAGGCTCAGATGAGGTTAAAGGAGGCCCTTCGACTTCGACATGTGTCCCCCTCCGGAC
F R V Y S N F L R G K L K L Y T G E A C -
CAGGACAGGGACAGATGACCAGGTCGAC
601 -----+-----+----- 629
GTCCTGTCCCCCTGTCTACTGGTCCAGCTG
R T G D R * -

FIG. 3b

REPLACEMENT SHEET

1 GGAATTCAACCACCATGGGGTGCACGAATGTCCTGCCTGGCTGTGGCTTCCTGTCCCT 60
 1-----+-----+-----+-----+-----+-----+
 1 CCTTAAGTGGTGGTACCCCCACGTGCTTACAGGACGGACCCGAAGAGGACAGGGA
 1 M G V H E C P A W L W L L S L -
 61 GCTGTCGCTCCCTCTGGGCCTCCCAGTCCTGGCGCCCCCCCCGCCCCACACGCCTCAT 120
 61-----+-----+-----+-----+-----+-----+
 61 CGACAGCGAGGGAGACCCGGAGGGTCAGGACCCCGGGGGGGGGGGGGTGGTGCAGGTA
 61 L S L P L G L P V L G A P P A P P R L I -
 121 CTGTGACAGCCGAGTCCTGGAGAGGTACCTTGGAGGCCAAGGAGGCCGAGAATATCAC 180
 121-----+-----+-----+-----+-----+-----+
 121 GACACTGTCGGCTCAGGACCTCTCCATGGAGAACCTCCGGTTCTCCGGCTCTTATAGTG
 121 C D S R V L E R Y L L E A K E A E N I T -
 181 GACGGGCTGTGCTGAACACTGCAGCTTGAATGAGAATATCACTGTCCCAGACACCAAAGT 240
 181-----+-----+-----+-----+-----+-----+
 181 CTGCCCGACACGACTTGTGACGTCGAACCTACTCTTATAGTGACAGGGTCTGTGGTTCA
 181 T G C A E H C S L N E N I T V P D T K V -
 241 TAATTTCTATGCCTGGAAGAGGATGGAGGTGGGGCAGCAGGCCGTAGAAGTCTGGCAGGG 300
 241-----+-----+-----+-----+-----+-----+
 241 ATTAAGATAACGGACCTTCTCCTACCTCCAGCCCCGTGTCGGCATCTCAGACCGTCCC
 241 N F Y A W K R M E V G Q Q A V E V W Q G -
 301 CCTGGCCCTGCTGCGAACGCTGTCCTGCGGGGCCAGGCCCTGTTGGTCAACTCTTCCCA 360
 301-----+-----+-----+-----+-----+-----+
 301 GGACCGGGACGACGCCCTCGACAGGACGCCCGGTCCGGACAACCAGTTGAGAAGGGT
 301 L A L L S E A V L R G Q A L L V N S S Q -
 361 GCCGTGGGAGCCCTGCACTGCAGCTGCATGTGGATAAGCCGTCACTGGCCTTCGCAGCCTCAC 420
 361-----+-----+-----+-----+-----+-----+
 361 CGGCACCCCTCGGGGACGTCGACGTACACCTATTCGGCAGTCACCGGAAGCGTCGGAGTG
 361 P W E P L Q L H V D K A V S G I R S L T -
 421 CACTCTGCTTCGGCTCTGGGAGCCAGAAGGAAGCCATCTCCCTCCAGATGCGGCCTC 480
 421-----+-----+-----+-----+-----+-----+
 421 GTGAGACGAAGCCCGAGACCTCGGGCTTCCTCGGTAGAGGGAGGTCTACGCCGGAG
 421 T L L R A L G A Q K E A I S P P D A A S -

FIG. 4a

REPLACEMENT SHEET

AGCTGCTCCACTCCGAACAATCACTGCTGACACTTCCGCAAACCTCTCCGAGTCTACTC
481 -----+-----+-----+-----+-----+-----+-----+ 540
TCGACGAGGTGAGGCTTGTAGTGACGACTGTGAAAGGCCTTGAGAAGGCTCAGATGAG
A A P L R T I T A D T F R K L F R V Y S -

CAATTTCCCTCCGGGAAAGCTGAAGCTGTACACAGGGAGGCCTGCAGGACAGGGACAG
541 -----+-----+-----+-----+-----+-----+-----+ 600
GTTAAAGGAGGCCCTTTCGACTTCGACATGTGTCCCCTCCGGACGTCCGTCCCCTGTC
N F L R G K L K L Y T G E A C R T G D R -

ATGACCAGGTCGAC
601 -----+--- 614
TACTGGTCCAGCTG
* -

FIG. 4b

REPLACEMENT SHEET

1 GGAATTCAACCACCATGGGGTGCACGAATGTCCTGCCTGGCTGTGGCTCTCCGTCCCT
 1 CTTAAGTGGTGGTACCCCCACGTGCTACAGGACGGACCGACACCGAAGAGGGACAGGGA 60
 1 M G V H E C P A W L W L L S L -

 61 GCTGTCGCTCCCTCTGGGCCTCCCAGTCCTGGCGCCCCCCCCGGCGCCGCCACTACGC
 61 CGACAGCGAGGGAGACCCGGAGGGTCAGGACCCGGGGGGGGCCGGCGGGTGTGCG 120
 61 L S L P L G L P V L G A P P G A A H Y A -

 121 CCCACCA CGCCTCATCTGTGACAGCCAGTCCTGGAGAGGTACCTCTGGAGGCCAAGGA
 121 GGGTGGTGC GGAGTAGACACTGTCGGCTCAGGACCTCTCCATGGAGAACCTCCGGTTCCT 180
 121 P P R L I C D S R V L E R Y L L E A K E -

 181 GGCGAGAATATCACGACGGCTGTGCTGAACACTGCAGCTTGAATGAGAATATCACTGT
 181 CCGGCTCTTATAGTGTGCTGCCGACACGACTTGTGACGTGAACTTACTCTTATAGTGACA 240
 181 A E N I T T G C A E H C S L N E N I T V -

 241 CCCAGACACCAAAAGTTAATTCTATGCCTGGAAGAGGATGGAGGTGGGGCAGCAGGCCGT
 241 GGGTCTGTGGTTCAATTAAAGATA CGGACCTCTCCTACCTCCAGCCCGTGTCCGGCA 300
 241 P D T K V N F Y A W K R M E V G Q Q A V -

 301 AGAAGTCTGGCAGGGCTGGCCCTGCTGCGGAAGCTGTCTGCAGGCCCTGTT
 301 TCTTCAGACCGTCCGGACCGGACGACAGCCTTCGACAGGACGCCCGGTCCGGGACAA 360
 301 E V W Q G L A L L S E A V L R G Q A L L -

 361 GGTCAACTCTTCCCAGCCGTGGAGCCCTGCAGCTGCATGTGGATAAGCCGTAGTGG
 361 CCAGTTGAGAAGGGTCGGCACCCCTCGGGGACGTGACGTACACCTATTTCGGCAGTCACC 420
 361 V N S S Q P W E P L Q L H V D K A V S G -

 421 CCTTCGCAGCCTCACCACTTGCTTCGGCTCTGGGAGCCAGAAGGAAGCCATCTCCCC
 421 GGAAGCGTCGGAGTGGTGAGACGAAGCCCGAGACCCCTCGGGTCTCCTCGGTAGAGGGG 480
 421 L R S L T T L L R A L G A Q K E A I S P -

FIG. 5a

REPLACEMENT SHEET

481 TCCAGATGCGGCCTCAGCTGCTCCACTCCGAACAATCACTGCTGACACTTCCGAAACT 540
-----+-----+-----+-----+-----+-----+-----+
AGGTCTACGCCGGAGTCGACGAGGTGAGGCTTGTAGTGACGACTGTGAAAGGCCTTGA
P D A A S A A P L R T I T A D T F R K L -

541 CTTCCGAGTCTACTCCAATTCCCTCCGGGAAAGCTGAAGCTGTACACAGGGGAGGCCTG 600
-----+-----+-----+-----+-----+-----+
GAAGGCTCAGATGAGGTTAAGGAGGCCCTTCGACTTCGACATGTGTCCCCCTCCGGAC
F R V Y S N F L R G K L K L Y T G E A C -

601 CAGGACAGGGACAGATGACCAGGTCGAC 629
-----+-----+-----+
GTCCTGTCCCCCTGTCTACTGGTCCAGCTG
R T G D R * -

FIG. 5b